

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/532,014  
Source: PCT  
Date Processed by STIC: 2/22/06

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PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/532,014

DATE: 02/22/2006

TIME: 08:26:00

Input Set : A:\Sequence-List.txt  
 Output Set: N:\CRF4\02222006\J532014.raw

3 <110> APPLICANT: Karolinska Innovations AB  
 4 Ingelman-Sundberg, Magnus  
 5 Karlgren, Maria  
 6 Gomez, Alvin  
 8 <120> TITLE OF INVENTION: Drug target in cancer therapy  
 10 <130> FILE REFERENCE: P05980PC00/HAM/em  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/532,014  
 C--> 12 <141> CURRENT FILING DATE: 2005-04-20  
 12 <150> PRIOR APPLICATION NUMBER: SE0203137-5  
 13 <151> PRIOR FILING DATE: 2002-10-24  
 15 <150> PRIOR APPLICATION NUMBER: US 60/420,787  
 16 <151> PRIOR FILING DATE: 2002-10-24  
 18 <160> NUMBER OF SEQ ID NOS: 10  
 20 <170> SOFTWARE: PatentIn version 3.1  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 27  
 24 <212> TYPE: DNA  
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 27 <220> FEATURE:  
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 29 <222> LOCATION: (1)..(27)  
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 37 <210> SEQ ID NO: 2  
 38 <211> LENGTH: 25  
 39 <212> TYPE: DNA  
 40 <213> ORGANISM: Homo sapiens  
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 W--> 43 <221> NAME/KEY: primer  
 44 <222> LOCATION: (1)..(25)  
 45 <223> OTHER INFORMATION:  
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 49 ctggatcagg gcgtccacat agctg 25  
 52 <210> SEQ ID NO: 3  
 53 <211> LENGTH: 23  
 54 <212> TYPE: DNA  
 55 <213> ORGANISM: homo sapiens  
 57 <220> FEATURE:  
 W--> 58 <221> NAME/KEY: primer  
 59 <222> LOCATION: (1)..(23)  
 60 <223> OTHER INFORMATION:  
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64 agctatgtgg acgcctgtat cca          23
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68 <211> LENGTH: 23
69 <212> TYPE: DNA
70 <213> ORGANISM: homo sapiens
72 <220> FEATURE:
W--> 73 <221> NAME/KEY: primer
74 <222> LOCATION: (1)..(23)
75 <223> OTHER INFORMATION:
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84 <212> TYPE: PRT
85 <213> ORGANISM: homo sapiens
87 <220> FEATURE:
88 <221> NAME/KEY: peptide
89 <222> LOCATION: (1)..(15)
90 <223> OTHER INFORMATION:
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95 Thr Met Arg Pro Arg Ala Gln Ala Leu Cys Ala Val Pro Arg Pro
96 1           5           10          15
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101 <212> TYPE: DNA
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116 <212> TYPE: DNA
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121 <222> LOCATION: (1)..(28)
122 <223> OTHER INFORMATION:
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132 <213> ORGANISM: homo sapiens
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136 Met Ala Leu Leu Leu Leu Leu Phe Leu Gly Leu Leu Gly Leu Trp Gly
137 1           5           10          15
  
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140 Leu Leu Cys Ala Cys Ala Gln Asp Pro Ser Pro Ala Ala Arg Trp Pro  
141 20 25 30  
144 Pro Gly Pro Arg Pro Leu Pro Leu Val Gly Asn Leu His Leu Leu Arg  
145 35 40 45  
148 Leu Ser Gln Gln Asp Arg Ser Leu Met Glu Leu Ser Glu Arg Tyr Gly  
149 50 55 60  
152 Pro Val Phe Thr Val His Leu Gly Arg Gln Lys Thr Val Val Leu Thr  
153 65 70 75 80  
156 Gly Phe Glu Ala Val Lys Glu Ala Leu Ala Gly Pro Gly Gln Glu Leu  
157 85 90 95  
160 Ala Asp Arg Pro Pro Ile Ala Ile Phe Gln Leu Ile Gln Arg Gly Gly  
161 100 105 110  
164 Gly Ile Phe Phe Ser Ser Gly Ala Arg Trp Arg Ala Ala Arg Gln Phe  
165 115 120 125  
168 Thr Val Arg Ala Leu His Ser Leu Gly Val Gly Arg Glu Pro Val Ala  
169 130 135 140  
172 Asp Lys Ile Leu Gln Glu Leu Lys Cys Leu Ser Gly Gln Leu Asp Gly  
173 145 150 155 160  
176 Tyr Arg Gly Arg Pro Phe Pro Leu Ala Leu Leu Gly Trp Ala Pro Ser  
177 165 170 175  
180 Asn Ile Thr Phe Ala Leu Leu Phe Gly Arg Arg Phe Asp Tyr Arg Asp  
181 180 185 190  
184 Pro Val Phe Val Ser Leu Leu Gly Leu Ile Asp Glu Val Met Val Leu  
185 195 200 205  
188 Leu Gly Ser Pro Gly Leu Gln Leu Phe Asn Val Tyr Pro Trp Leu Gly  
189 210 215 220  
192 Ala Leu Leu Gln Leu His Arg Pro Val Leu Arg Lys Ile Glu Glu Val  
193 225 230 235 240  
196 Arg Ala Ile Leu Arg Thr Leu Leu Glu Ala Arg Arg Pro His Val Cys  
197 245 250 255  
200 Pro Gly Asp Pro Val Cys Ser Tyr Val Asp Ala Leu Ile Gln Gln Gly  
201 260 265 270  
204 Gln Gly Asp Asp Pro Glu Gly Leu Phe Ala Glu Ala Asn Ala Val Ala  
205 275 280 285  
208 Cys Thr Leu Asp Met Val Met Ala Gly Thr Glu Thr Thr Ser Ala Thr  
209 290 295 300  
212 Leu Gln Trp Ala Ala Leu Leu Met Gly Arg His Pro Asp Val Gln Gly  
213 305 310 315 320  
216 Arg Val Gln Glu Glu Leu Asp Arg Val Leu Gly Pro Gly Arg Thr Pro  
217 325 330 335  
220 Arg Leu Glu Asp Gln Gln Ala Leu Pro Tyr Thr Ser Ala Val Leu His  
221 340 345 350  
224 Glu Val Gln Arg Phe Ile Thr Leu Leu Pro His Val Pro Arg Cys Thr  
225 355 360 365  
228 Ala Ala Asp Thr Gln Leu Gly Gly Phe Leu Leu Pro Lys Gly Thr Pro  
229 370 375 380  
232 Val Ile Pro Leu Leu Thr Ser Val Leu Leu Asp Glu Thr Gln Trp Gln  
233 385 390 395 400  
236 Thr Pro Gly Gln Phe Asn Pro Gly His Phe Leu Asp Ala Asn Gly His

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237 405 410 415  
240 Phe Val Lys Arg Glu Ala Phe Leu Pro Phe Ser Ala Gly Arg Arg Val  
241 420 425 430  
244 Cys Val Gly Glu Arg Leu Ala Arg Thr Glu Leu Phe Leu Leu Phe Ala  
245 435 440 445  
248 Gly Leu Leu Gln Arg Tyr Arg Leu Leu Pro Pro Pro Gly Val Ser Pro  
249 450 455 460  
252 Ala Ser Leu Asp Thr Thr Pro Ala Arg Ala Phe Thr Met Arg Pro Arg  
253 465 470 475 480  
256 Ala Gln Ala Leu Cys Ala Val Pro Arg Pro  
257 485 490  
260 <210> SEQ ID NO: 9  
261 <211> LENGTH: 2432  
262 <212> TYPE: DNA  
263 <213> ORGANISM: homo sapiens  
265 <220> FEATURE:  
266 <221> NAME/KEY: promoter  
267 <222> LOCATION: (1)..(137)  
268 <223> OTHER INFORMATION:  
271 <220> FEATURE:  
272 <221> NAME/KEY: exon  
273 <222> LOCATION: (138)..(1608)  
274 <223> OTHER INFORMATION:  
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278 gccctgcaaa ctgctcggttc cacattctcg ggggtgggtggg gtgggtgggg tgccgggcacg 60  
280 ccctcccgcg gaggcctata aagggtgcggg ggggacgggg cccaggaggg gatggagcc 120  
282 tcaccagcca cgtcctc atg gcc ctg ctg ttg ctg ttc ctg ggc ctc 170  
283 Met Ala Leu Leu Leu Leu Phe Leu Gly Leu  
284 1 5 10  
286 ctg ggg ctc tgg ggg ctc tgc gcc tgc gac ccc tcc cca 218  
287 Leu Gly Leu Trp Gly Leu Leu Cys Ala Cys Ala Gln Asp Pro Ser Pro  
288 15 20 25  
290 gct gcc cgg tgg ccc ccc ggg cct cgc ccg ctg ccg ctc gtc ggg aac 266  
291 Ala Ala Arg Trp Pro Pro Gly Pro Arg Pro Leu Pro Leu Val Gly Asn  
292 30 35 40  
294 ctg cac ttg ctg cgt ctg tcg caa cag gac cgg tcc ctg atg gag ctc 314  
295 Leu His Leu Leu Arg Leu Ser Gln Gln Asp Arg Ser Leu Met Glu Leu  
296 45 50 55  
298 tca gaa cgc tac ggg ccg gtg ttc acc gtg cac ctg ggg cgc cag aag 362  
299 Ser Glu Arg Tyr Gly Pro Val Phe Thr Val His Leu Gly Arg Gln Lys  
300 60 65 70 75  
302 acg gtg gtg ctg acg ggg ttc gag ggc gtc aaa gag ggc ctg ggc ggc 410  
303 Thr Val Val Leu Thr Gly Phe Glu Ala Val Lys Glu Ala Leu Ala Gly  
304 80 85 90  
306 ccc ggg cag gag ctg gcc gac cgg cct ccc atc gcc atc ttc cag ctc 458  
307 Pro Gly Gln Glu Leu Ala Asp Arg Pro Pro Ile Ala Ile Phe Gln Leu  
308 95 100 105  
310 atc cag cga ggt gga ggc atc ttc ttc tca tct ggg ggc cgc tgg agg 506  
311 Ile Gln Arg Gly Gly Ile Phe Phe Ser Ser Gly Ala Arg Trp Arg

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312	110	115	120	
314	gct gcc cgc cag ttc acg gtg cgt gcc ctg cac agc ctg ggc gtg ggc			554
315	Ala Ala Arg Gln Phe Thr Val Arg Ala Leu His Ser Leu Gly Val Gly			
316	125	130	135	
318	cgg gag ccg gtg gct gac aag att ctg cag gag ctg aaa tgc ctc tct			602
319	Arg Glu Pro Val Ala Asp Lys Ile Leu Gln Glu Leu Lys Cys Leu Ser			
320	140	145	150	155
322	ggg cag ctg gat ggc tac aga ggc cgg ccc ttc ccg ctg gcc cta ctg			650
323	Gly Gln Leu Asp Gly Tyr Arg Gly Arg Pro Phe Pro Leu Ala Leu Leu			
324	160	165	170	
326	ggc tgg gct ccc tcc aat atc acc ttc gcg ctc ctc ttc ggc cgc cga			698
327	Gly Trp Ala Pro Ser Asn Ile Thr Phe Ala Leu Leu Phe Gly Arg Arg			
328	175	180	185	
330	ttt gac tac cgg gac ccc gtg ttt gtg tcc ctg ctg ggt ctc atc gat			746
331	Phe Asp Tyr Arg Asp Pro Val Phe Val Ser Leu Leu Gly Leu Ile Asp			
332	190	195	200	
334	gag gtc atg gtc ctc ttg ggg tcc cct ggc ctg cag ctg ttc aac gtc			794
335	Glu Val Met Val Leu Leu Gly Ser Pro Gly Leu Gln Leu Phe Asn Val			
336	205	210	215	
338	tac cca tgg ctc ggg gcc ctg ctc cag ctg cac cgg ccc gtc ctg cgc			842
339	Tyr Pro Trp Leu Gly Ala Leu Leu Gln Leu His Arg Pro Val Leu Arg			
340	220	225	230	235
342	aag atc gag gag gtc cgt gcc att ctg agg acc ctc ctg gag gcg cgg			890
343	Lys Ile Glu Glu Val Arg Ala Ile Leu Arg Thr Leu Leu Glu Ala Arg			
344	240	245	250	
346	agg ccc cac gtg tgc ccg ggg gac ccc gtg tgc agc tat gtg gac gcc			938
347	Arg Pro His Val Cys Pro Gly Asp Pro Val Cys Ser Tyr Val Asp Ala			
348	255	260	265	
350	ctg atc cag cag gga cag ggg gat gac ccc gag ggc ctg ttt gct gag			986
351	Leu Ile Gln Gln Gly Gln Asp Asp Pro Glu Gly Leu Phe Ala Glu			
352	270	275	280	
354	gcc aac gcg gtg gcc tgc acc ctg gac atg gtc atg gcc ggg acg gag			1034
355	Ala Asn Ala Val Ala Cys Thr Leu Asp Met Val Met Ala Gly Thr Glu			
356	285	290	295	
358	acg acc tcg gcc acg ctg cag tgg gcc gca ctt ctg atg ggc cgg cac			1082
359	Thr Thr Ser Ala Thr Leu Gln Trp Ala Ala Leu Leu Met Gly Arg His			
360	300	305	310	315
362	ccg gac gtg cag ggc cgg gtg cag gag gag cta gac cgc gtg ctg ggc			1130
363	Pro Asp Val Gln Gly Arg Val Gln Glu Glu Leu Asp Arg Val Leu Gly			
364	320	325	330	
366	cct ggg cgg act ccc ccg ctg gag gac cag cag gct ctg ccc tac aca			1178
367	Pro Gly Arg Thr Pro Arg Leu Glu Asp Gln Gln Ala Leu Pro Tyr Thr			
368	335	340	345	
370	agc gcc gtg ctc cac gag gtg cag cgg ttc atc acg ctc ctg ccc cac			1226
371	Ser Ala Val Leu His Glu Val Gln Arg Phe Ile Thr Leu Leu Pro His			
372	350	355	360	
374	gtg ccc cgc tgc acc gcg gcc gac aca cag ctg ggc ggc ttc ctg ctc			1274
375	Val Pro Arg Cys Thr Ala Ala Asp Thr Gln Leu Gly Gly Phe Leu Leu			
376	365	370	375	

**VERIFICATION SUMMARY**  
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TIME: 08:26:01

Input Set : A:\Sequence-List.txt  
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:28 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1  
L:33 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:30  
L:43 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2  
L:48 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:45  
L:58 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:63 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:60  
L:73 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
L:78 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:75  
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